

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1875 (-)_2124388_2124831
Date	Fri Aug 2 13:30:49 BST 2019
Unique Job ID	e0973f3c03a2cef6

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1w9aa_	Alignment		100.0	24	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
2	d2asfa1	Alignment		100.0	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
3	d1rfea_	Alignment		100.0	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
4	c3f7eB_	Alignment		100.0	24	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeq_3380 f420 reductase
5	c4zkyB_	Alignment		100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5-phosphate oxidase; PDBTitle: structure of f420 binding protein, msmeq_6526, from mycobacterium2 smegmatis
6	c2iabB_	Alignment		99.9	21	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a protein with fmn-binding split barrel fold2 (np_828636.1) from streptomyces avermitilis at 2.00 a resolution
7	d2fhqa1	Alignment		99.9	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
8	c3tgvD_	Alignment		99.9	16	PDB header: heme binding protein Chain: D: PDB Molecule: heme-binding protein hutz; PDBTitle: crystal structure of hutz,the heme storsge protein from vibrio2 cholerae
9	d2i02a1	Alignment		99.9	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
10	c3ec6A_	Alignment		99.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: general stress protein 26; PDBTitle: crystal structure of the general stress protein 26 from bacillus2 anthracis str. Sterne
11	c2re7A_	Alignment		99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase related2 protein (psyc_0186) from psychrobacter arcticus 273-4 at 2.50 a3 resolution

12	d1vl7a_	Alignment		99.9	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
13	d2hq7a1	Alignment		99.9	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
14	c2htdB_	Alignment		99.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: predicted flavin-nucleotide-binding protein from cog3576 PDBTitle: crystal structure of a putative pyridoxamine 5'-phosphate oxidase2 (ldb0262) from lactobacillus delbrueckii subsp. at 1.60 a resolution
15	c3db0B_	Alignment		99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: lin2891 protein; PDBTitle: crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution
16	d2fg9a1	Alignment		99.9	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
17	c5escD_	Alignment		99.9	17	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
18	d2hq9a1	Alignment		99.9	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
19	d2htia1	Alignment		99.9	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
20	c2htia_	Alignment		99.9	10	PDB header: fmn-binding protein Chain: A: PDB Molecule: bh0577 protein; PDBTitle: crystal structure of a flavin-nucleotide-binding protein (bh_0577)2 from bacillus halodurans at 2.50 a resolution
21	c3u0iA_	Alignment	not modelled	99.9	16	PDB header: unknown function Chain: A: PDB Molecule: probable fad-binding, putative uncharacterized protein; PDBTitle: crystal structure of a probable fad-binding, putative uncharacterized2 protein from brucella melitensis
22	c3u34D_	Alignment	not modelled	99.9	15	PDB header: protein binding Chain: D: PDB Molecule: general stress protein; PDBTitle: crystal structure of the general stress fmn/fad binding protein from2 the phytopathogen xanthomonas citri
23	c2q9kA_	Alignment	not modelled	99.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution
24	c3dmbA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative general stress protein 26 with a pnp-oxidase like PDBTitle: crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
25	c3fkhB_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution
26	c6eciQ_	Alignment	not modelled	99.8	19	PDB header: fad-binding protein Chain: Q: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn-binding PDBTitle: structure of the fad binding protein msmeq_5243 from mycobacterium2 smegmatis
						PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase-

27	c2hhzA_	Alignment	not modelled	99.8	19	related; PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
28	d1ty9a_	Alignment	not modelled	99.8	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
29	d1t9ma_	Alignment	not modelled	99.8	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
30	c2ig6B_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nimc/nima family protein; PDBTitle: crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution
31	d1dnla_	Alignment	not modelled	99.8	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
32	c2qeaB_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative general stress protein 26; PDBTitle: crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution
33	d1flma_	Alignment	not modelled	99.8	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
34	d1nrqa_	Alignment	not modelled	99.8	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
35	c1nrqA_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
36	d2arza1	Alignment	not modelled	99.8	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
37	c4hmwB_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phzg from burkholderia lata 383
38	c3cp3A_	Alignment	not modelled	99.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae
39	d2a2ja1	Alignment	not modelled	99.8	24	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
40	c5bncB_	Alignment	not modelled	99.8	21	PDB header: heme binding protein Chain: B: PDB Molecule: heme binding protein msmeq_6519; PDBTitle: structure of heme binding protein msmeq_6519 from mycobacterium2 smegmatis
41	c2a2jA_	Alignment	not modelled	99.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
42	c3dnhB_	Alignment	not modelled	99.8	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein atu2129; PDBTitle: the crystal structure of the protein atu2129 (unknown function) from2 agrobacterium tumefaciens str. c58
43	c2ou5B_	Alignment	not modelled	99.7	9	PDB header: flavoprotein Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn-binding; PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase-related fmn-2 binding protein (jann_0254) from jannaschia sp. ccs1 at 1.60 a3 resolution
44	d2fura1	Alignment	not modelled	99.7	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
45	c3gasA_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
46	c4ybnB_	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin-nucleotide-binding protein; PDBTitle: structure of the fad and heme binding protein msmeq_4975 from2 mycobacterium smegmatis
47	d1ci0a_	Alignment	not modelled	99.6	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
48	c2i51B_	Alignment	not modelled	99.6	13	PDB header: flavoprotein Chain: B: PDB Molecule: uncharacterized conserved protein of cog5135; PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase-related, fmn2 binding protein (npun_f5749) from nostoc punctiforme pcc 73102 at3 1.40 a resolution
49	d2vpaa1	Alignment	not modelled	99.5	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
50	c6rk0A_	Alignment	not modelled	99.5	17	PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the flavocytochrome anf3 from azotobacter vinelandii
51	d1xhna1	Alignment	not modelled	99.4	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
52	c2o15B_	Alignment	not modelled	99.4	12	PDB header: transcription regulator Chain: B: PDB Molecule: pai 2 protein; PDBTitle: crystal structure of a protease synthase and sporulation

						negative2 regulatory protein pai 2 from bacillus stearotherophilus
53	c4n7rD	Alignment	not modelled	99.0	15	PDB header: oxidoreductase/protein binding Chain: D: PDB Molecule: genomic dna, chromosome 3, p1 clone: mxl8; PDBTitle: crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein
54	c3h96B	Alignment	not modelled	98.5	15	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
55	c3r5yC	Alignment	not modelled	98.4	21	PDB header: unknown function Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420
56	c3r5zB	Alignment	not modelled	98.4	21	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
57	c3r5wO	Alignment	not modelled	98.3	18	PDB header: oxidoreductase Chain: O: PDB Molecule: deazaflavin-dependent nitroreductase; PDBTitle: structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420
58	c3ba3A	Alignment	not modelled	98.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase-like protein; PDBTitle: crystal structure of pyridoxamine 5'-phosphate oxidase-like protein2 (np_783940.1) from lactobacillus plantarum at 1.55 a resolution
59	c4y9iA	Alignment	not modelled	98.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
60	d2ptfa1	Alignment	not modelled	97.2	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
61	c2ptfB	Alignment	not modelled	96.6	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein mth_863; PDBTitle: crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn
62	d2imla1	Alignment	not modelled	96.0	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
63	c3b5mD	Alignment	not modelled	95.5	21	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
64	d1ejea	Alignment	not modelled	93.7	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
65	d2nr4a1	Alignment	not modelled	90.8	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
66	c3fgeA	Alignment	not modelled	90.3	9	PDB header: oxidoreductase Chain: A: PDB Molecule: putative flavin reductase with split barrel domain; PDBTitle: crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution
67	c3bpbK	Alignment	not modelled	88.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase component b; PDBTitle: crystal structure of nitrilotriacetate monooxygenase component b from2 bacillus cereus
68	c3e4vA	Alignment	not modelled	88.5	14	PDB header: flavoprotein Chain: A: PDB Molecule: nadh:fmn oxidoreductase like protein; PDBTitle: crystal structure of nadh:fmn oxidoreductase like protein in complex2 with fmn (yp_544701.1) from methylobacillus flagellatus kt at 1.40 a3 resolution
69	c4z85A	Alignment	not modelled	88.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitrobenzoate nitroreductase; PDBTitle: crystal structur of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa
70	c2d5mA	Alignment	not modelled	75.7	14	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: flavodoxin of desulfovibrio vulgaris (miyazaki f)
71	c4f07A	Alignment	not modelled	66.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: styrene monooxygenase component 2; PDBTitle: structure of the styrene monooxygenase flavin reductase (smob) from2 pseudomonas putida s12
72	c3bnkB	Alignment	not modelled	65.3	5	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: x-ray crystal structure of flavodoxin from methanosarcina2 acetivorans
73	c3cb0B	Alignment	not modelled	52.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxyphenylacetate 3-monooxygenase; PDBTitle: cobr
74	d1i0ra	Alignment	not modelled	51.4	8	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
75	d1lusca	Alignment	not modelled	49.1	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
76	c3rh7A	Alignment	not modelled	48.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (sma0793)

						from2 sinorhizobium meliloti 1021 at 3.00 a resolution
77	c4xhyA_	Alignment	not modelled	47.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase domain protein, fmn-binding protein; PDBTitle: nadh:fmn oxidoreductase from paracoccus denitrificans
78	c2d38A_	Alignment	not modelled	45.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical nadh-dependent fmn oxidoreductase; PDBTitle: the crystal structure of flavin reductase hpac complexed with nadp+
79	c2qckA_	Alignment	not modelled	43.1	9	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase domain protein; PDBTitle: crystal structure of flavin reductase domain protein (yp_831077.1)2 from arthrobacter sp. fb24 at 1.90 a resolution
80	c3hmzA_	Alignment	not modelled	36.9	6	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase domain protein, fmn-binding; PDBTitle: crystal structure of a fmn-binding domain of flavin reductases-like2 enzyme (sba1_0626) from shewanella baltica os155 at 1.50 a resolution
81	d1rz0a_	Alignment	not modelled	34.4	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
82	c2ecrA_	Alignment	not modelled	34.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase component (hpac) of 4-hydroxyphenylacetate PDBTitle: crystal structure of the ligand-free form of the flavin reductase2 component (hpac) of 4-hydroxyphenylacetate 3-monooxygenase
83	d1wgba_	Alignment	not modelled	32.2	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
84	c3pftA_	Alignment	not modelled	28.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase; PDBTitle: crystal structure of untagged c54a mutant flavin reductase (dszd) in2 complex with fmn from mycobacterium goodii
85	c4l82D_	Alignment	not modelled	27.5	6	PDB header: oxidoreductase Chain: D: PDB Molecule: rifea.00250.a; PDBTitle: structure of a putative oxidoreductase from rickettsia felis
86	c2opkC_	Alignment	not modelled	16.6	50	PDB header: isomerase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
87	c2r6vA_	Alignment	not modelled	15.4	0	PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein ph0856; PDBTitle: crystal structure of fmn-binding protein (np_142786.1) from pyrococcus2 horikoshii at 1.35 a resolution
88	c2r0xA_	Alignment	not modelled	11.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: possible flavin reductase; PDBTitle: crystal structure of a putative flavin reductase (ycdh, hs_1225) from2 haemophilus somnus 129pt at 1.06 a resolution
89	c3nfwB_	Alignment	not modelled	9.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin reductase-like, fmn-binding protein; PDBTitle: crystal structure of nitrilotriacetate monooxygenase component b2 (a0r521 homolog) from mycobacterium thermoresistibile
90	c3k87B_	Alignment	not modelled	8.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: chlorophenol-4-monooxygenase component 1; PDBTitle: crystal structure of nadh:fad oxidoreductase (tftc) - fad2 complex
91	c5ag8A_	Alignment	not modelled	8.5	21	PDB header: hydrolase Chain: A: PDB Molecule: gingipain r2; PDBTitle: crystal structure of a mutant (665i6h) of the c-terminal2 domain of rgpb
92	c4kt0F_	Alignment	not modelled	7.5	11	PDB header: electron transport Chain: F: PDB Molecule: photosystem i subunit iii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
93	c6igzF_	Alignment	not modelled	6.7	22	PDB header: plant protein Chain: F: PDB Molecule: psaf; PDBTitle: structure of psi-lhci
94	d1jb0f_	Alignment	not modelled	6.4	22	Fold: Single transmembrane helix Superfamily: Subunit III of photosystem I reaction centre, PsaF Family: Subunit III of photosystem I reaction centre, PsaF
95	c6ijjF_	Alignment	not modelled	6.3	22	PDB header: membrane protein Chain: F: PDB Molecule: psaf; PDBTitle: photosystem i of chlamydomonas reinhardtii
96	c6fosF_	Alignment	not modelled	5.2	22	PDB header: photosynthesis Chain: F: PDB Molecule: photosystem i reaction center subunit ii; PDBTitle: cyanidioschyzon merolae photosystem i
97	d1pgl22	Alignment	not modelled	5.2	16	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
98	d1ny722	Alignment	not modelled	5.1	22	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP